



+

5/22

G1071 (95)
T06584 (102)
SAP1 (103)
G1072 (96)
AAK00433 (104)
G1068 (97)
G1069 (42)
G21533 (6)
G3456 (14)
G3401 (38)
G3402 (101)
G3403 (22)
G2157 (98)
G3556 (40)
G1067 (4)
G2156 (8)
G3400 (30)
G3399 (10)
G1073 (2)
G2789 (99)
G596 (100)
G1070 (48)
G3405 (28)
G3404 (32)
G1075 (54)
G1076 (54)
G3460 (18)
G3459 (16)
G3458 (24)
G3406 (26)
G3407 (34)
G1945 (44)
G2155 (46)
G3408 (20)
BAB64709 (105)
G3462 (36)

MDRRDAMGLSGSG
MDGREAMAFSG

MEAKDVSPLVTVPAPAAAAAPPPAAPPPSQPPPLPFAQQAPPPAA
MDSREIHHQQQQQQQQQQQQQQQQQQ

MD
MD
MDPVQSH
MDPVTAS
MDPVTAA

FIG. 5A

+

+

6/22

G1071 (95)
T06584 (102)
SAP1 (103)
G1072 (96)
AAK00433 (104)
G1068 (97)
G1069 (42)
G2153 (6)
G3456 (14)
G3401 (38)
G3402 (101)
G3403 (22)
G2157 (98)
G3556 (40)
G1067 (4)
G2156 (8)
G3400 (30)
G3399 (10)
G1073 (2)
G2789 (99)
G596 (100)
G1070 (48)
G3405 (28)
G3404 (32)
G1075 (52)
G1076 (54)
G3460 (18)
G3459 (16)
G3458 (24)
G3406 (26)
G3407 (34)
G1945 (44)
G2155 (46)
G3408 (20)
BAB64709 (105)
G3462 (36)

SYIHRGLSGSPPTFHGSPQQQQLRHLPNQNSPFGSGSTGFGSPSLHG
GPGSYLHRGGVEAAGSGSGGFQVPPGFRALPNNGIIAQPNVRAQGGNGD
MEQPNNDGNNGGSCYRQLPNQ-----
METSDRISPGGIGAEVPSAYHMAPRPSDS-----
NPAAAPMRLSFDOMAGKAPGGEQQHHHPGPMLYAAAPAGGAAPPQGGN
HLQQQQQPPPGMLMSHHNSYNRNPNAAAVLMGHTNSTSQAMHQRLPFGG
MANPWTNQSLAGMVDH-----
MANPWTGQVNLSGLETTTPGSSQ--LKKPDLHI
MANRWTGSGVLENSGHS-----

MGLPEQPSG-----
MANPWWVGNVAIGGVESPVTSSAPSLHHRNSNN

MEGGYEQGGGASRYFHNLFERPEIHHQQLQPQGGINLIDQHHH
MDGGYDQSGGASRYFHNLFERPELHHQLQ-PQPQLHPLPQPQP
MAGMDPTGGGGGVAHYLHMLRAQQH--QPLSPAGDVKA
MAGMDPGGGAGAGSSRYFHLLLRPQQPSPLSPTSHTVVKM

EVS-----RSHTPQFLSSD-HQYHHQNA-----GRQKRGRE-----
QVS-----RSLPPPFLSRDLHLHPHQFO-----HQQQQQQNHGHDI
GSQ-----SSLPPPFFHARDFQLHLQQQQQEFFLHHHQQRNQTGDQQG
IHG-----HHLPPPFTTRDFHHLQQQQQHQLHLKTEDDQGGTGPVFG-
AAHGGHHHHHFGAPPVAAFHHHPFHGGGAHYPAAFQFQEEQQQLVA
MAGLDLG-TTSRYVHNVDGG-GGGQFTTDNHHEDDG-----
MAGLDLG-TAFRYVNHQLHR-PDLHLHNSSSDDVTP-----
MAGLDLG-SASRFVQN-LHL-PDLHLQQNYQQPR-----
MAGLDLG-SASRFVQN-LHR-PDLHLQQNYQQHQDQ-----
MAGLDLG-SASHFVHRLER-PDLEDDEQQDQDNN-----
MAGLDLGTAAATRYVHQLHHLHPDLQLQHSYAKQHEP-----
MAGLDLG-----TSYLHHHQLHLRHDDGGAG-----MK

MSFCERDMNKESMYQERDDMAGIRFATPPLPQQQQQ-----

FIG. 5B

+

7/22

G1071	(95)	DPSLATAAGGAGALPHHIGVNMIA	PPPPSETPMKKRGRPRKYQDGSV	
T06584	(102)	TSSMFSLPQSHADFNHDI	SVGASSGAPSEPVKKRGRPRKYGPDGSVS	
SAP1	(103)	-----SPANGVPNSTT	NSTHSPNESVKRKRGRPR-----KYGTP	
G1072	(96)	-----PANQFMGLSLP	MEAPMPSSGEASGKKRRGRPRK-----YEANGA	
AAK00433	(104)	VMGMGELMRKKRGRPRKYA	PDGSMALALAPISSASGGAAPPPPPGHQPH	
G1068	(97)	SMSPHQPQQHQYHHPQ	QQQIDQKLTLESFGFTSPLPSASNSYGGGNEG	
G1069	(42)	-----SVSSGHHQH	HHHQLTKGDLGIAMNQSDNDQDE-----EDDPR	
G2153	(6)	SMNMAMDSGHNHHH	HHQEVNNDNN-----DDDRDNLSGD-----DHEPR	
G3456	(14)	-----MKK-PDLGFS	MNESTVTGNHIG-----EEDEDRENSD-----EPR	
G3401	(38)	MASKEPSG	-----DHDHEMNGTSAG-----GGEPK	
G3402	(101)	MASKEPSGDH	-----DHDHEMNGTSAG-----GGEPK	
G3403	(22)	-----SSGPKAELP	VAKEPEASPTGGA-----AADHADENNESG-----GGEPR	
G2157	(98)	NPPTMTRSDPRLDH	DFTTNNSGSPNTQTQSQEEQNSRDE-----QPAVE	
G3556	(40)	MGSIDGHS	LQQHQGYSHGGAGGSNEEEASPPP-----GGGSA	
G1067	(4)	QHQQHQQQQP	SDDSR-----ESDSNKDHHQQG-----RPDSD	
G2156	(8)	QPQPQQN	-----ESDS-NKD-----PGSD	
G3400	(30)	ERSMLSPDES	PGADAD-----LGSDH-PTSSAMVA-----AED-S	
G3399	(10)	EHSKMS	PDKSPVGEGDHAGSGSGVGGDHQPSSAMVP-----VEGGS	
G1073	(2)	MELNRSEAD	EAK-----AETPTGATSS-----ATA--	
G2789	(99)	-----EEGVEPN	-----NIGEDLATFPSSG-----EE--	
G596	(100)	DQHRIGGLKRDR	-----DADIDPNEHSSAGKDQSTPSSG-----GESGG	
G1070	(48)	GSGGNROI	KMDREETSDNIDNIANNSGSEKDDIHGGS-----GEGGG	
G3405	(28)	-----SRGT	KRDHDD--DENSGNHGSGGDGDALVPPS-----GGGPD	
G3404	(32)	AAAAAGGMA	KQELVDESNTINSGSGNSGGEQRQSSG-----EEQHQ	
G1075	(52)	-----GAGGNHHH	--HHNHHHQQGLDLIASNDN-SG-----LGGGG	
G1076	(54)	-----GAGMGH	FTVDDENNHNHQQGLDLASGGSGSS-----GGGGG	
G3460	(18)	-----HKRD	SEEQETPPNPGTALAPFDND-DDKS-----QGLEL	
G3459	(16)	-----QHQR	DLEEQTTPN-HRMGAPFDDDDSDRS-----PGLLEL	
G3458	(24)	-----LNNH	EGLDLVTPNS-----G--	
G3406	(26)	-----SDDDP	NGSGGGNSNGGPYGDHDGSSSSSGP-----ATDGA	
G3407	(34)	-----SDDG	GHDDLSPGS-----GGGGPSS-----TAGGA	
G1945	(44)	GEYREQS	NEMFSLPHHQQQQQQQQSHSLTSHFHLSS-----TVTPT	
G2155	(46)	MLSKLPTQR	-----HLHLSP-----SSP--	
G3408	(20)	-----QQLV	ECFSDEVDSRSGGGE--MKDAVGS	SGQLV-----VVG
BAB64709	(105)	MADEGSSRAELI	-----EASPA	
G3462	(36)	TRSNSNTNANTNTNTT	EEEEVSRDNGEDQNQLGS-----HEGSE	

FIG. 5C

+

8/22

G1071	(95)	SLALS	SSSVSTITPNN	-- SNKR	-- GRGRPPGSGKK	-- QRMAS	V	GELMPSS
T06584	(102)	LKLTPMS	APANSTQDSGTPSEKR	-- GRGRPPGSGKK	-- GRGRPPGSGKK	-- QOLAAL	G	GDWMTSS
SAP1	(103)	EQAAA	AKRLS	-- APKKRDS	ASGVASVSS	KKSPIA	ALGN	--
G1072	(96)	PLP	SSSVPL	-- VKKR	-- VRGKLNGFDMK	-- KMHKT	I	GFHSSGE
AAK00433	(104)	GFSISS	PASD	-- PNAK	-- RRGRPPGSGKK	-- KQFEAL	G	SWG
G1068	(97)	GGGDS	AGANANSSD	-- PPAKR	-- NRGRPPGSGKK	-- QLDAL	G	GTG
G1069	(42)	EGA	-- VEVV	-- NRR	-- PRGRPPGSGKNK	-- PKAPI	F	VTRD
G2153	(6)	E	-- GAVEAP	-- TRR	-- PRGRPPGSGKNK	-- PKPPI	F	VTRD
G3456	(14)	E	-- GAIDVA	-- TTR	-- PRGRPPGSGKNK	-- PKPPI	F	VTRD
G3401	(38)	D	-- GAVVTG	-- RNRR	-- PRGRPPGSGKNK	-- PKPPI	F	VTRD
G3402	(101)	D	-- GAVVTG	-- RNRR	-- PRGRPPGSGKNK	-- PKPPI	F	VTRD
G3403	(22)	E	-- GAVVAA	-- PNRR	-- PRGRPPGSGKNK	-- PKPPI	F	VTRD
G2157	(98)	P	-- GSGSGS	-- TGRR	-- PRGRPPGSGKNK	-- PKSPVV	V	VTKE
G3556	(40)	T	-- GS	-- AGRR	-- PRGRPPGSGKNK	-- PKPPV	V	VTRE
G1067	(4)	PN	-- TSSSA	-- PGKR	-- PRGRPPGSGKNK	-- AKPPI	I	VTRD
G2156	(8)	P	-- VTSGS	-- TGKR	-- PRGRPPGSGKNK	-- PKPPI	I	VTRD
G3400	(30)	G	-- GSGSGG	-- PMRR	-- PRGRPPGSGKNK	-- PKPPI	I	VTRD
G3399	(10)	GS	AGSGSGG	-- PTRR	-- PRGRPPGSGKNK	-- PKPPI	I	VTRD
G1073	(2)	S	-- GSSG	-- RR	-- PRGRPPGSGKNK	-- PKPPI	I	VTRD
G2789	(99)	--	-- NI	-- KRRR	-- PRGRPPGSGKNK	-- PKAPI	I	VTRD
G596	(100)	G	-- GGDNH	-- ITRR	-- PRGRPPGSGKNK	-- PKPPI	I	VTRD
G1070	(48)	G	-- SGGDHQ	-- MTRR	-- PRGRPPGSGKNK	-- PKPPI	I	VTRD
G3405	(28)	G	-- AGS-ES	-- ATRR	-- PRGRPPGSGKNK	-- PKPPI	I	VTRD
G3404	(32)	Q	-- GAAAPV	-- VIRR	-- PRGRPPGSGKNK	-- PKPPV	I	VTRD
G1075	(52)	G	-- GSGDL	-- VMRR	-- PRGRPPGSGKNK	-- PKPPV	I	VTRE
G1076	(54)	H	-- GGGDV	-- VGRR	-- PRGRPPGSGKNK	-- PKPPV	I	VTRE
G3460	(18)	A	-- SGPGDI	-- VGRR	-- PRGRPPGSGKNK	-- PKPPV	I	VTRE
G3459	(16)	T	-- SGPGDI	-- VGRR	-- PRGRPPGSGKNK	-- PKPPV	I	VTRE
G3458	(24)	--	-- PGDV	-- VGRR	-- PRGRPPGSGKNK	-- PKPPV	I	VTRE
G3406	(26)	V	-- GPGDV	-- VARR	-- PRGRPPGSGKNK	-- PKPPV	I	VTRE
G3407	(34)	G	-- IGGGEV	-- VARR	-- PRGRPPGSGKNK	-- PKPPV	I	VTRE
G1945	(44)	V	-- DDSIE	-- VVRR	-- PRGRPPGSGKNK	-- PKPPV	F	VTRD
G2155	(46)	--	-- SME	-- TVGR	-- PRGRPPGSGKNK	-- PKAPI	F	VT
G3408	(20)	D	-- GASIE	-- VAKK	-- PRGRPPGSGKNK	-- PKPPV	I	VTRE
BAB64709	(105)	P	-- ALDLP	-- PPRK	-- PRGRPPGSGKNK	-- PKPPV	V	VTRE
G3462	(36)	P	-- GS	-- SGR	-- PRGRPPGSGKNK	-- PKPPI	V	IFL

AT-hook domain

FIG. 5D

+

9/22

G1071	(95)	SGMSFTPHVIAVSLIGEDIASKVIAFSQOQGPRAICVLSAS
T06584	(102)	AGIAFSFPHVITIAAGEDIAAKLLLSQORRALCILSGT
SAP1	(103)	MGQSFSPHIIIVAAAGEDVQKIMFVQOSKREICVISAS
G1072	(96)	RFGVGGVGGVSNFTPHVITMNTGEDITMRISFSQOQGPRAICILSAN
AAK00433	(104)	IAFTPHIILVMKAGEDVASKIMAFSQOQGPRTVCILSAN
G1068	(97)	GVGFTPHVIEVKITGEDIAKILAFNQGPRAICILSAT
G1069	(42)	SPNALRSHVLEISDGSADVADTIAHFSRRRQRGVCVLSGT
G21533	(6)	SPNALKSHVMEIASGTDVIEETLAFARRRQRGICILSGN
G3456	(14)	SPNALRSHVMEIAVGADVADCVAQFARRRQRGVSILSGS
G3401	(38)	SPNALRSHVMEVAGGADVAAESIAHFARRRQRGVCVLSGA
G3402	(101)	SPNALRSHVMEVAGGADVAAESIAHFARRRQRGVCVLSGA
G3403	(22)	SPNALRSHVMEVAGGADVADAIQFSRRRQRGVCVLSGA
G2157	(98)	SPNSLOSHVLEIATGADVAAESINAFARRRQRGVSILSGS
G3556	(40)	SPNAMRSHVLEIASGADIIEAIAGFSSRRRQRGVSILSGS
G1067	(4)	SPNALRSHVLEVSFGADIIVESVTYARRRQRGVSILSGN
G2156	(8)	SPNMLRSHVLEVSFGADIIVESVTYARRRQRGVSILSGN
G3400	(30)	SPNAFHSHVLEVAAGTDIIEVCVEFARRRQRGVCVLSGG
G3399	(10)	SPNALHSHVLEVAAGGADVVDCAVEYARRRQRGVCVLSGG
G1073	(2)	SPNMLRSHVLEVTSGSDISEAVSTYARRRQGVCIISGT
G2789	(99)	SANAFRCHVMEITINACDVMEESLAFARRRQRGVCVLTGN
G596	(100)	SANALKSHVMEVANGCDVMEESVTFARRRQRGICVLSGN
G1070	(48)	SANALRTHVMEIGDGCDDLVESVATFARRRQRGVCMST
G3405	(28)	SANTLRTHVMEVAGGCDIISESITTFARRRQRGVCVLSGA
G3404	(32)	SASALRAHVLEVASGCDLVDSVATFARRRQRGVCVLSAT
G1075	(52)	SANTLRAHILEVSGSGCDVFECSISTYARRRQRGICVLSGT
G1076	(54)	SANTLRAHILEVINGSGCDVFDCAVATYARRRQRGICVLSGS
G3460	(18)	SANTLRAHILEVSGSGSDVFDCAVATYARRRQRGICVLSGS
G3459	(16)	SANTLRAHILEVSGSGSDVFDCAVATYARRRQRGICVLSGS
G3458	(24)	SANTLRAHILEVSGSGCDVFEESVATYARRRQRGICVLSGS
G3406	(26)	SANTLRAHILEVSGSGCDVFEESVATYARRRQRGICVLSGS
G3407	(34)	SANALRAHILEVAAGCDVFEALTA YARRRQRGVCVLSAA
G1945	(44)	IDPMSPIYLEVPSGNDVMEAINRFCRRKSTGVCVLSGS
G2155	(46)	IDPMSPIYLEVPSGNDVMEAINRFCRRKSTGVCVLSGS
G3408	(20)	PAAAMRPHVIEIPGGRDVAEALRFSRRNLGICVLAGT
BAB64709	(105)	SEAMRPVVLELGAAGCEVAATAVAAFAARRRQGVSVLCCR
G3462	(36)	SPNALRSHVLEIASGRDVAESIAAFANRRHRGVSVLSGS

second conserved domain

FIG. 5E

+

10/22

G1071	(95)	GAVSTATLILQP	---	SASPG	---	ATKVEGRFEILALSL	SYIVATDG
T06584	(102)	GIASKVTLRQP	---	ASTNAG	---	VTVYEGKFOILSLSGSYLVSEDDG	---
SAP1	(103)	GSVSSALRQP	---	ASSGG	---	SVTVYEGRFDILSLSGSFIHAE	---
G1072	(96)	GVIISNVTLRQP	---	DISCGG	---	TLTVYEGRFEILSLSGSFMETENQG	---
AAK00433	(104)	GAIISNVTLRQP	---	ATISGG	---	LTVYEGRFEILSLSGSFLAEDGD	---
G1068	(97)	GAVTNMMLRQAN	---	NSNPTG	---	TVKYEGRFEILSLSGSFLNSESNG	---
G1069	(42)	GSVANVTLRQ	---	AAAPGG	---	VVSLQGRFEILSLTGAFLLPGE	---
G2153	(6)	GTVANVTLRQP	STAA	VAAAPGGAA	---	VVALQGRFEILSLTGSLFLPGE	---
G3456	(14)	GTVINVTLRQP	---	TAPGAV	---	MALHGRFDILSLTGSLFLPGE	---
G3401	(38)	GTVIDVALROP	---	AAPSA	---	VVALRGRFEILSLTGTFLLPGE	---
G3402	(101)	GTVIDVALROP	---	AAPSA	---	VVALRGRFEILSLTGTFLLPGE	---
G3403	(22)	GTVANVALROP	---	SAPGA	---	VVALHGRFEILSLTGTFLLPGE	---
G2157	(98)	GLVTNVTLRQ	AAS	---	GG	VVSLRQGRFEILSMCGAFLPTSG	---
G3556	(40)	GAVTNVTLRQ	AGTG	---	AA	AVALLRGRFEILSMCGAFLPAP	---
G1067	(4)	GTVSNVTLRQP	VTPGNGGVSG	GGG	---	VVTLHGRFEILSLTGTVLLPPE	---
G2156	(8)	GTVANVTLRQP	ATTAHANG	GGG	---	VVALHGRFEILSLTGTVLLPPE	---
G3400	(30)	GAVANVTLRQP	G	---	ASPPGSL	VATMRGRFEILSLTGTVLLPPE	---
G3399	(10)	GAVNVTLRQP	G	---	ASPPGSM	VATLRGRFEILSLTGTVLLPPE	---
G1073	(2)	GAVTNVTIROP	---	AAPAGG	---	VITLHGRFDILSLTGTVLLPPE	---
G2789	(99)	GAVTNVTIROP	---	PGG	---	VVSLHGRFEILSLSGSFLPPE	---
G596	(100)	GAVTNVTIROP	AS	---	VPGGGS	VVNLHGRFEILSLSGSFLPPE	---
G1070	(48)	GAVTNVTIROP	GS	---	HPSPGS	VVSLHGRFEILSLSGSFLPPE	---
G3405	(28)	GTVTNVTLRQ	---	PASQGA	---	VVALHGRFEILSLSGSFLPPE	---
G3404	(32)	GAVTNVSVROP	---	GAGPGA	---	VVNLHGRFDILSLSGSFLPPE	---
G1075	(52)	GTVTNVTIROP	---	TAAGA	---	VVTLRGTTFEILSLSGSFLPPE	---
G1076	(54)	GTVTNVTIROP	---	SAAGA	---	VVTLQGTTFEILSLSGSFLPPE	---
G3460	(18)	GTVTNVTIROP	---	AAAGA	---	VVRLHGRFEILSLSGSFLPPE	---
G3459	(16)	GTVTNVTIROP	---	AAAGA	---	VVTLHGRFEILSLSGSFLPPE	---
G3458	(24)	GTVTNVTIROP	S	---	AAAGA	VVTLHGRFEILSLSGSFLPPE	---
G3406	(26)	GTVTNVTIROP	S	---	APAGA	VVSLHGRFEILSLSGSFLPPE	---
G3407	(34)	GTVANVTLRQP	QSAQ	PGPASEA	---	VATLHGRFEILSLAGSFLPPE	---
G1945	(44)	GSVANVTLRQP	S	---	PAALGS	TIHFKGFDLLSVSATFLPPE	PPTS
G2155	(46)	GSVANVTLRQP	S	---	PAAPGS	TIHFKGFDLLSVSATFLPPE	PPTS
G3408	(20)	GAVANVTLRQP	SP	---	GVPGSAP	PAIVFHGRYEILSLSATFLPPE	AMSSV
BAB64709	(105)	GTVAAVTLRLP	---	TSPPA	---	AVKLHGRFEVLSLSTGTVLLPPE	SAAGEG
G3462	(36)	GTVANVTLRQ	AAP	---	AG	VITLHGRFEILSLSGAFLPPE	---

second conserved domain

FIG. 5F

+

+

11/22

G1071 (95)
T06584 (102)
SAP1 (103)
G1072 (96)
AAK00433 (104)
G1068 (97)
G1069 (42)
G2153 (6)
G3456 (14)
G3401 (38)
G3402 (101)
G3403 (22)
G2157 (98)
G3556 (40)
G1067 (4)
G2156 (8)
G3400 (30)
G3399 (10)
G1073 (2)
G2789 (99)
G596 (100)
G1070 (48)
G3405 (28)
G3404 (32)
G1075 (52)
G1076 (54)
G3460 (18)
G3459 (16)
G3458 (24)
G3406 (26)
G3407 (34)
G1945 (44)
G2155 (46)
G3408 (20)
BAB64709 (105)
G3462 (36)

--SFRNRITGNLSVSLASPDGRVIGGAI GGPLIAASPVQVI VGSFI--WAAP
--PTNRITGGISVLSLRDGHVIGGSVA-MLIAGSPIQLVVCSEFV-YGGG
--FGGRITGGLSVCLSSDGOIIGGVGGPILIAAATIQVI VGTFFV-VETIK
--SKGRITGGMVSLSLAGPDGRVVGCGVAGLLIAATPIQV VGSFI-TSDQ
--TRSRITGGLSVALAGSDGRVLGGCVAGMLMAATPVQV VASFI-AEGK
--TVTKITGNLSVSLAGHEGRIVGGCVDCMLVAGSQVQVI VGSFVPDGRK
--SPPGSTGLTVYLAGVQGOVVGGSVVGPLLAIGSV M V I A A T F S - N A T Y
--APPGSTGLTIYLAGGQGOVVGGSVVGPLMAAGPVM L I A A T F S - N A T Y
--SPPGATGLTIYLAGGQGOVVGGEVVGPLV A A G P V L V M A A T F S - N A T Y
--APPGSTGLTVYLAGGQGOVVGGSVVGTLT A A G P V M V I A S T F A - N A T Y
--APPGSTGLTVYLAGGQGOVVGGSVVGSLI A A G P V M V I A S T F A - N A T Y
--SPAAAGLTIYLAGAQGOVVGGSVAGP L I A S G P V I V I A A T F C - N A T Y
--APPGATGLAVYLAGGQGOVVGGSVMGELI A S G P V M V I A A T F G - N A T Y
--APPGAGGLSIFLAGGQGOVVGGSVAP L I A S A P V I L M A A S F S - N A V F
--APPGSGGLSIFLSGMQGOVIGGNVAP L V A S G P V I L M A A S F S - N A T F
--APPSASGLTVFLSGGQGOVVGGSVAGQ L I A A G P V L M A A S F A - N A V Y
--APPGASGLTVFLSGGQGOVIGGSVGP L V A A G P V L M A A S F A - N A V Y
--APPGAGGLTVYLAGGQGOVVGGNVAGSLI A S G P V L M A A S F A - N A V Y
--APPAASGLTVYLAGGQGOVIGGSVGP L I A S S P V V M A A S F G - N A S Y
--APPAASGLTIYLAGGQGOVIGGSVVGPLM A S G P V V I M A A S F G - N A A Y
--APPTATGLSVYLAGGQGOVVGGSVVGPL L C A G P V V M A A S F S - N A A Y
--APPEATGLTVYLAGGQGOVVGGSVVGAL T A A G P V V I M A A S F A - N A V Y
--APPSATGLTVYVSGGQGOVVGGTVAGP L I A V G P V V I M A A S F G - N A A Y
--APPGATSLTIIFLAGAQGOVVGGNVVGELM A A G P V M V M A A S F T - N V A Y
--APPGATSLTIIFLAGGQGOVVGGSVVGELT A A G P V I V I A A S F T - N V A Y
--APPGATSLTIYLAGGQGOVVGGNVVGELT A A G P V I V I A A S F T - N V A Y
--APPGATSLTIYLAGGQGOVVGGNVIGELT A A G P V I V I A A S F T - N V A Y
--APPGATSLTVFLGGQGOVVGGNVVGPLV A S G P V I V I A S S F T - N V A Y
--APPGATSLTIIFLAGGQGOVVGGNVVGAL I Y A A G P V I V I A A S F A - N V A Y
--APPGATSLAIFLAGGQGOVVGGSVAGAL I A A G P V V V A A S F S - N V A Y
L--SPPVSNFTVSLAGPQGOIIGGFVAGP L I S A G T V V I A A S F N - N P S Y
L--SPPVSNFTVSLAGPQGVIGGFVAGP L V A A G T V Y F V A T S F K - N P S Y
APQA A V A A A G L S I S L A G P H G O I V G G A V A G P L Y A A T T V V V A A A F T - N P T F
A--APPPP--FVSLSLAGAGGOVIGGTLAGE M I T A D G L V V A A T F G - S A E V
--SPSGATGLTVYLAGGQGOVVGGNVAGSLV A S G P V M V I A A T F A - N A T Y

second conserved domain

FIG. 5G

+

+

12/22

G1071	(95)	KIKSKKREEE	ASEVVOETD	DHHVLDNNN	NT
T06584	{102}	SKVKTKQG	MITNGES	SEPHNDNLG	SPASA
SAP1	{103}	KDANVEAAS	GKSPSPNGG	ASAPGLSFRSPADSGIOM	
G1072	(96)	QDHQKPRQR	VEHAPAAVMS	VPPPPSPPPPAASVFSPT	
AAK00433	{104}	KSKPVETRKVEP	MSAPPOMATYVPAPVASPPSEGT	SGS	
G1068	(97)	QKOSAGRAQN	TPEPASAPANMLSF	GGPGSPRSQQQHSSE	
G1069	{42}	ERLPMEEE	E-DGGCSR	QIHGGDSPP	RIGSNL
G2153	(6)	ERLPLEEEFAA	ERGGGCGSGGVVPG	QLGGG-SPL	SSGAGG
G3456	{14}	ERLPLEDD	DQEQHCGG	GGSP-QE	KNGGPG
G3401	{38}	ERLPDQEE	EEEAAG	GMMAPPP	LMAG--
G3402	{101}	ERLPDQED	QEEAAG	GMMAPPP	LMAG--
G3403	{22}	ERLPLEE	EEGSGPP	MPGGAEP	LMAGGH
G2157	{98}	ERLPIEEQ	QEQPLOED	GKKQKEEND	NESGNN
G3556	{40}	ERLPDQEE	EGAVLSGSE	GAAQOMEQQ	SS
G1067	{4}	ERLPLEE	EEGCGG	GGG-GGPPQM	QAPSASPP
G2156	{8}	ERLPLE-DEG	EGEGCGEVGEGG	GPP--	PATSSSPP
G3400	{30}	ERLPDGEDPE	AEAAATPPGDAAQ	PTGPPPPQQ	PTASQSSEV
G3399	{10}	ERLPLEGEE	VAAPAAAGEAQDQ	VAQSAQPPGQQ	PAASQSSGV
G1073	{2}	ERLPLEE	TPPRTTGVQQQ	QPEASQSSEVT	GSGAQACES
G2789	{99}	ERLPLEE	TEREIDGNA	ARAIGTQTQ	---
G596	{100}	ERLPLEEDQ	EEQTAGAVANNID	GNA	---
G1070	{48}	ERLPLEED	---	MQTPVHCGG	---
G3405	{28}	ERLPLEDD	---	LLAAQQA	---
G3404	{32}	ERLPLEDD	---	PPQHMA	---
G1075	{52}	ERLPLEDEHEH	---	LQSGGG	---
G1076	{54}	ERLPLEED	---	QQLGGSN	---
G3460	{18}	ERLPLEED	---	HQQLQIQSPAATS	---
G3459	{16}	ERLPLEED	---	QHQQLQIQPPATTS	---
G3458	{24}	ERLPLEDE	---	SMQMQGQSSAGD	---
G3406	{26}	ERLPLEED	---	APPOAGLQMQPGGA	---
G3407	{34}	ERLPLEDE	---	VPPAPAGSDQGG	---
G1945	{44}	ERLPLEEEQK	---	HSAGTGER	---
G2155	{46}	ERLPLEEE	---	RNSAEGEE	---
G3408	{20}	ERLPADDDASVS	---	VSVSLSGSG	---
BAB64709	{105}	ERLPADDEDE	---	ATGSRGEE	---
G3462	{36}	ERLPLEDDGE	---	EEMVQVQQQ	---

FIG. 5H

+

+

13/22

G1071	(95)	ISPVP	---QQPNQNI	IWSTGSRQ	---MDMRHAHAD	IDLMRG
T06584	{102}	PPDQN	---YISPTGMW	PGSQPSD	---MKSAPAH	TGIDLTRG
SAP1	{103}	GGGNGPFL	IQNRTMHT	MEWIGSADHG	---MHQSPENG	DYDHIPD
G1072	{96}	NPDR	---QPPSSF	GISWINGQDMP	---RNSATDINIS	SLPVD
AAK00433	{104}	SDDSG	---SPINHS	GMENHSGQQQ	HHQHQH	QHMPPAYASGGWSLSAHHQ
G1068	{97}	SSEEN	---ESNSPL	HRNNSNNHGI	FGNSTPQ	PLHQIPMQYQNLWP
G1069	{42}	PDLSC	---MAGPGYN	MPPHIIPNG	---AGQL	GHEPYTWVHA
G2153	{6}	GDGN	---QGLPVYN	MPGNLVSNGSG	---GGQMS	QOEAYGWAQA
G3456	{14}	EASSS	---ISVYNN	NVPSLGLPNGQH	---LNHEAYSS	PWGHSFA
G3401	{38}	-AADP	---LLF	---GGGMHDAGL	---AAWHHAR	PPP
G3402	{101}	-AADP	---LLF	---GGGMHDAGL	---AAWHHAR	PPP
G3403	{22}	GIADP	---SALPMFN	LPNSNGLGGGD	---GFPWAAH	PRP
G2157	{98}	GNEGS	---MQPPMYN	MPFNIPNGH	---QMAQHD	VYWGGPPP
G3556	{40}	G-GAV	---VPPPMYA	AVQOTPPHDM	---FGQWGHAA	VARPP
G1067	{4}	SGVTG	---OQQLGG	NVGGYG	---FSGDPHLL	GWGAGTSPSRPP
G2156	{8}	SGAG	---OQQLRG	NMSGYDQ	---FAGDPHLL	GWGAAAAAAPP
G3400	{30}	TAGDG	---GGGGLGMY	---LGGHVS	QYQQQQL	PCPDNFGSWSGIRP
G3399	{10}	TGGDGT	GGAGGMSLYN	LAGNVGGY	---QLP	---GDNFGGWSGAGAG
G1073	{2}	NLQGG	---NGGGVAF	YNLGMNMF	---QFSG	---GDIYGMSSGSGGGGG
G2789	{99}	QLMQD	---ATSF	FIGSPSNI	INSVSL	---P
G596	{100}	QLMQD	---PTSF	FIGGLPPN	ILMNSVQL	---P
G1070	{48}	QHQQ	---AMSGH	QGLPPN	ILGNSVQL	---QQHDQSYWSTG
G3405	{28}	AGGAV	---DPSLF	QGLPPN	ILGNSVQL	---PPEAA
G3404	{32}	LPPHQ	---QPILOD	HLPHNLMNGIHL	---PGDAA	YGWTS
G1075	{52}	GGGG	---LPFF	NLPM	SMP	---QIGVESWQGNHA
G1076	{54}	AGGG	---G	LPFFNLPM	NQPN	---VQLPVEGWPGNSG
G3460	{18}	PDPSS	---G	LPFFNLPL	NQON	---VQLPPF
G3459	{16}	PDPSS	---G	LPFFNLPL	NQON	---VQLPVEGWAVNPA
G3458	{24}	PDPSS	---G	LPFFNLPL	NQON	---VQLPVEGWAGNSG
G3406	{26}	DPSAA	---G	LPFFNLPL	NQON	---VQLPVEGWAGNSG
G3407	{34}	GGAAT	---GGLP	FFNMPFGMPP	---MPVD	GHAGWPGAGVG
G1945	{44}	AGSGG	---ESCGV	SMYSCHMGGG	---DVIWAPT	ARAP
G2155	{46}	G	---	ES	---	DVIWAPT
G3408	{20}	QLRRPP	PHLSAAA	AVSAAQ	PFVEPCGAP	MYACHPOQOEVMWPPPARTPHPP
BAB64709	{105}	VGLLG	YGGVG	VAGASGGQ	VGRHQ	QQQ
G3462	{36}	GLGEQ	---	VSM	PMYNLPPN	LHNG

FIG. 51

+

